

Result No.	Score	Query Match	Length	DB ID	Description
C 1	35	100.0	638	4 XLU88561	U98561 Xenopus laevis

Fri Oct 1 16:47:15 1999

	Location/Qualifiers
FEATURES	
source	I..638 /organism="Xenopus laevis" /db_xref="taxon:89355" /cell_type="oocyte"
gene	107...583 /gene="ubc9"
CDS	107...583 /gene="Ubc9" /note="UBC9" /codon_start=1 /product="E2 ubiquitin conjugating enzyme"
	/protein_id="AA857736.1" /db_xref="PID:g2078331" /db_xref="GI:2078331"
	/translation="MSGIALSRUAQERKAWRKDHPGFVAVPTKNPDGTMNLMWECIA IPFGKTPEGGGLFKRLMLFVKDYSPSKPKFPPLFHNVTPSGTVCLSILEDKRDI WRPAIRIKQLLIGIQELLNEPNIDPQAQEAYTIYQNRYVEYEKRVRQAQAKKFAPS"
BASE COUNT	214 A 131 C 147 G 146 T
ORIGIN	
	Query Match 100.0%; Score 35; DB 4; Length 638; Best Local Similarity 100.0%; Pred. NO. 0.078;
Matches	35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 gactcgagtcgacatgcgatgtttttttttttt 35
Dd	638 GACTCGAGTCGACATGCAGTTTTTTTITTTI 604
RESULT	2
A24382	
LOCUS	A24382 35 bp DNA PAT 21-MAR-1995
DEFINITION	dlt17 adaptor primer.
ACCESSION	A24382
NID	g904477
VERSION	A24382.1 GI:904477
KEYWORDS	. synthetic construct. artificial sequence.
SOURCE	synthetic construct. synthetic construct. artificial sequence.
REFERENCE	1 (bases 1 to 35) Sarmientos,P., De Taxis du Poet.P., Nitti,G. and Scacheri,E. Anti-thrombin polypeptides Patent: EP 0501821-A 22 02-SEP-1992;
TITLE	FARMITALIA CARLO ERBA S.r.L
JOURNAL	
FEATURES	location/Qualifiers 1..35 /organism="synthetic construct" /db_xref="taxon:32630"
BASE COUNT	5 A 5 C 5 G 20 T
ORIGIN	
	Query Match 100.0%; Score 35; DB 5; Length 35; Best Local Similarity 100.0%; Pred. No. 0.095;
Matches	35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 gactcgagtccacatgcgatgtttttttttttt 35
Dd	1 GACTCGAGTCGACATCATGTCTTTTITTTTITT 35
RESULT	3
A27645	
LOCUS	A27645 35 bp DNA PAT 04-JUN-1995
DEFINITION	Hybrid dTL7-adaptor primer.
ACCESSION	A27645
NID	g1248461
VERSION	A27645.1 GI:1248461
KEYWORDS	. synthetic construct.
SOURCE	.

[illegible]

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Query Match      100.0%; Score 35; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 35: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS I13679 35 bp DNA
DEFINITION Sequence 35 from patent US 5439820.
PAT 08-AUG-1995

KEYWORDS
Unknown
SOURCE

ORGANISM	Unknown.	Unclassified
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ADHORS	SARRENCOS, A., J. C. SANCHEZ AND J. L. GARCIA-LEON, 1987.
TITLE	Anti-thrombin polypeptides
PATENT:	US 5A20820-A 25 08 AUG-1995.
JOURNAL	

JOURNAL Patent: US 3455020 A 31 06 Nov 1970,
 FEATURES Location/Qualifiers
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 source
 /organism="unknown"
 5 2 5 2 20 +

[illegible]

Query Match	100.0%;	Score 35;	DB 5;	Length 35;
Best Local Similarity	100.0%;	Pred. No. 0.095;		

Matches	35;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Qy 1 gactcgagtcgacatcgaattttttttttttttttttttt 35

Db 1 GATCGAGTCGACATCGATTTT TTTT TTTT TTTT 35

RESULT 13
T24027

I24027		PAT	21-NOV-1998
LOCUS			
124027			
Coverage	0 from patient HG 554110	DNA	
SEQUENCE			

DEFINITION	Sequence 9 from patent US 5,541,111.
ACCESSION	I24027

NID	g1603897
VERSION	I24027.1
GI:1603897	

KEYWORDS
SOURCE
UNKNOWN

ORGANISM	Unknown.	Unidentified
ORGANISM	Unknown.	Unidentified

REFERENCE

AUTHORS Siegall, C.B.
TITLE Cloning and expression of a gene encoding bryodin 1 from Bryopsis

JOURNAL
dioica
Patent: US 5541110-A 9 30-JUL-1996;

FEATURES	Location/Qualifiers
source	1 35

source	1. 100	2. 100	3. 100	4. 100	5. 100	6. 100	7. 100	8. 100	9. 100	10. 100	11. 100	12. 100	13. 100	14. 100	15. 100	16. 100	17. 100	18. 100	19. 100	20. 100	21. 100	22. 100	23. 100	24. 100	25. 100	26. 100	27. 100	28. 100	29. 100	30. 100	31. 100	32. 100	33. 100	34. 100	35. 100	36. 100	37. 100	38. 100	39. 100	40. 100	41. 100	42. 100	43. 100	44. 100	45. 100	46. 100	47. 100	48. 100	49. 100	50. 100	51. 100	52. 100	53. 100	54. 100	55. 100	56. 100	57. 100	58. 100	59. 100	60. 100	61. 100	62. 100	63. 100	64. 100	65. 100	66. 100	67. 100	68. 100	69. 100	70. 100	71. 100	72. 100	73. 100	74. 100	75. 100	76. 100	77. 100	78. 100	79. 100	80. 100	81. 100	82. 100	83. 100	84. 100	85. 100	86. 100	87. 100	88. 100	89. 100	90. 100	91. 100	92. 100	93. 100	94. 100	95. 100	96. 100	97. 100	98. 100	99. 100	100. 100
source	1. 100	2. 100	3. 100	4. 100	5. 100	6. 100	7. 100	8. 100	9. 100	10. 100	11. 100	12. 100	13. 100	14. 100	15. 100	16. 100	17. 100	18. 100	19. 100	20. 100	21. 100	22. 100	23. 100	24. 100	25. 100	26. 100	27. 100	28. 100	29. 100	30. 100	31. 100	32. 100	33. 100	34. 100	35. 100	36. 100	37. 100	38. 100	39. 100	40. 100	41. 100	42. 100	43. 100	44. 100	45. 100	46. 100	47. 100	48. 100	49. 100	50. 100	51. 100	52. 100	53. 100	54. 100	55. 100	56. 100	57. 100	58. 100	59. 100	60. 100	61. 100	62. 100	63. 100	64. 100	65. 100	66. 100	67. 100	68. 100	69. 100	70. 100	71. 100	72. 100	73. 100	74. 100	75. 100	76. 100	77. 100	78. 100	79. 100	80. 100	81. 100	82. 100	83. 100	84. 100	85. 100	86. 100	87. 100	88. 100	89. 100	90. 100	91. 100	92. 100	93. 100	94. 100	95. 100	96. 100	97. 100	98. 100	99. 100	100. 100

BASE COUNT	3 4	3 5	3 6	3 7	20 3
ORIGIN					

Query Match	100.0%	score 35;	DB 5;	Length 35;
Best local similarity	100.0%	Pred. No.	0.095;	

Matches	35;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Qy 1 gactcgagtcgacatcgattttttttttttttttttt 35

Db 1 GACTCGAGTCGACATCGATTTTTTTTTTTTTTTTTTTT 35

RESULT 14
T2028A

40707T

Search completed: October 1, 1999, 15:34:59
Job time: 6202 sec


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Db 1 GACTCGAGTCGACATCGATTTTTTTTTTTTTTTT 35
RESULT 9
Q84786
ID Q84786 standard; DNA; 35 BP.
AC Q84786;
DT 17-AUG-1995 (first entry)
DE PTK22 reverse-transcription primer.
KW Protein-tyrosine-kinase; PTK; discoidin domain receptor; cancer;
KW breast tumor; mamma carcinoma; diagnosis; prognosis; therapy; ss.
OS Synthetic.
PN WO9502187-A.
PD 19-JAN-1995.
PF 08-JUL-1994; G01480.
PR 09-JUL-1993; GB-014271.
PA (CANC-) CANCER RES INST.
PA (WELL ) WELLCOME FOUND LTD.
PI Barker KT, Crompton MR, Gusterson BA, Martindale JE;
PI Mitchell PJ, Page MJ, Spence P;
PI WPI; 95-066991/09.
DR Method for screening substances, using protein tyrosine kinase -
PT for potential utility as therapeutic agents for cancer
PS Disclosure; Page 34; 51pp; English.
CC cDNA derived from tumor metastatic tissue was amplified using
CC primers (given in 084783-84) based on sequences (R71101, R71103)
CC associated with protein-tyrosine-kinases (PTK). Novel PTK22 was
CC identified in an isolated subclone. The 3' sequence of PTK22 was
CC obtained by reverse transcription (using the primer of 084786) and
CC PCR amplification (primers 084787-88) Of RNA of human breast
CC carcinoma cell line MDA MG 468. The partial DNA sequence of PTK22
CC is given in 084782. 5 A; 5 C; 5 G; 20 T;
SQ Sequence 35 BP; 5 A; 5 C; 5 G; 20 T;

Query Match 100.0%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gactcgagtcgacatcgattttttttttttttttttt 35
|||||
Db 1 GACTCGAGTCGACATCGATTTTTTTTTTTTTTTT 35

RESULT 10
Q90167
ID Q90167 standard; DNA; 35 BP.
AC Q90167;
DT 01-NOV-1995 (first entry)
DE Pollen allergen gene primer 8.
KW Japanese cedar; pollen; allergen; allergy; therapy; diagnostic;
KW desensitizer; Cryptomeria japonica; polymerase chain reaction;
KW PCR; primer; ss.
OS Synthetic.
PN EP-65500-A.
PD 31-MAY-1995.
PF 03-NOV-1994; 308117.
PR 05-NOV-1993; JP-299151.
PR 20-DEC-1993; JP-344596.
PR 27-DEC-1993; JP-346814.
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PI Kurimoto M, Namba M, Torigoe K;
PI WPI; 95-195588/26.
DR New Japanese cedar pollen allergen polypeptide - and DNA coding for it,
PT useful for treatment and diagnosis of cedar pollen allergy
PS Disclosure; Page 11; 41pp; English.
CC The primers given in 090166-69, based on a portion of cDNA clone
CC SC09 or on previously isolated sequences, were used for the PCR
CC amplification of cDNA derived from Japanese cedar pollen, to obtain
CC clone SC50 bearing a partial sequence (nt 1-198 of the sequence
CC given in 090156) of the pollen allergen gene.
CC Sequence 35 BP; 5 A; 5 C; 5 G; 20 T;
SQ Sequence 35 BP; 5 A; 5 C; 5 G; 20 T;

Query Match 100.0%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gactcgagtcgacatcgattttttttttttttttttt 35
|||||
Db 1 GACTCGAGTCGACATCGATTTTTTTTTTTTTTTT 35

RESULT 11
Q89878
ID Q89878 standard; DNA; 35 BP.
AC Q89878;
DT 31-JAN-1997 (Revised)
DT 25-OCT-1995 (first entry)
DE PCR primer for cloning bryodin-2.
KW Ribosome inactivating protein; cell death; proliferation; tumour;
KW cancer; virus; malaria; trypanosomiasis; inflammation; autoimmune;
KW disease; purging; bone marrow; ss.
OS Synthetic.
PN WO9511977-A.
PD 04-MAY-1995.
PF 25-OCT-1994; U12382.
PR 25-OCT-1993; US-141891.
PR 20-OCT-1994; US-324301.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA Gawlak SL, Marquardt H, Siegall CB;
PI WPI; 95-178870/23.
DR New ribosome inactivating protein bryodin-2 and related
PT conjugates - for killing target cells, e.g. in treatment of
PT cancer, also related nucleic acid, vectors and transformed cells
PT Disclosure; Page 43; 81pp; English.
PS The sequence is that of a PCR primer used to isolate a ribosome
CC of the protein with a ligand may be used to kill target cells (i.e. those
CC to which the ligand component binds specifically) or to inhibit
CC proliferation of tumour cells. Typical applications include the
CC treatment of cancer, viral infections, malaria, trypanosomiasis,
CC inflammatory or autoimmune diseases, including in vitro purging of e.g.
CC bone marrow.
CC See also Q89874-86.
CC Updated 31-JAN-1997 due to incorrect cross reference numbers.
CC Sequence 35 BP; 5 A; 5 C; 5 G; 20 T;
SQ Sequence 35 BP; 5 A; 5 C; 5 G; 20 T;

Query Match 100.0%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gactcgagtcgacatcgattttttttttttttttttt 35
|||||
Db 1 GACTCGAGTCGACATCGATTTTTTTTTTTTTTTT 35

RESULT 12
T05321
ID T05321 standard; DNA; 35 BP.
AC T05321;
DT 13-APR-1996 (first entry)
DE Oligonucleotide probe for human prostacyclin-synthase.
KW DNA probe; prostacyclin-synthase; PCR; polymerase chain reaction;
KW DNA primer; prostaglandin I2; circulatory disease; therapeutic;
KW diagnosis; gene therapy; ss.
OS Synthetic.
PN WO9530013-A1.
PD 09-NOV-1995.
PF 27-APR-1995; J00838.
PR 28-APR-1994; JP-114316.
PA (TANA/) TANABE T.
PI Tanabe T;
PI WPI; 95-393084/50.
PT Human prostacyclin synthase and DNA encoding it - useful in the

```



```

KEYWORDS  EST.
SOURCE      human.
ORGANISM    Homo sapiens

REFERENCE   1 (bases 1 to 337)
AUTHORS     Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
             Buit,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
             White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
             Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
             Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
             Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
             Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
             Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
             Phillips-Caia,A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
             Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
             Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
             Dinke,D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A.,
             He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
             Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
             Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
             Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseitine,W.A., Fields,C.,
             Fraser,C.M. and Venter,J.C.
TITLE       Initial assessment of human gene diversity and expression patterns
             based upon 83 million nucleotides of cDNA sequence
JOURNAL     Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE     96026280
COMMENT     On Sep 12, 1996 this sequence version replaced gi:11406936.
             Other ESTs: EST46035 THC125647
             Contact: Kerlavage, AR
             Bioinformatics
             The Institute for Genomic Research
             9712 Medical Center Drive, Rockville, MD 20850 USA
             Tel: 3018699056
             Fax: 3018699423
             Email: arkerlav@tigr.org
             For clone availability, additional sequence and expression
             information related to this EST, please check the TIGR Human Gene
             Index (http://www.tigr.org/tdb/hgi/hgi.html)
             Seq primer: ML3-21.
             Location/Qualifiers
               1. .337
               /organism="Homo sapiens"
               /db_xref="ATCC (inhost):142407"
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               /dev_stage="Fetus"
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BASE COUNT 63 a 88 c 95 g
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Query Match 100.0%; Score 35; DB 32; Length 337;
Best Local Similarity 100.0%; Pred. NO. 1.1;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gactcgagtcgacatcgatttttttttttttttttt 35
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Db 4 GACTCGAGTCGACATCGATCGATTTT TTTT TTTT 38

RESULT 2
AI295887/c 678 bp mRNA EST 01-DEC-1998
LOCUS LP09649.5prime LP Drosophila melanogaster larval-early pupal p0n2
DEFINITION Drosophila melanogaster cDNA clone LP09649 5prime, mRNA sequence.
ACCESSION AI295887
NID 93945294
VERSION AI295887.1 GI:3945294
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Buit,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitchhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips-Caia,A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dinke,D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseitine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT On Sep 12, 1996 this sequence version replaced gi:11406936.
Other ESTs: EST46035 THC125647
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: ML3-21.
Location/Qualifiers
1. .337
/organism="Homo sapiens"
/db_xref="ATCC (inhost):142407"
/db_xref="taxon:9606"
/clone_lib="Fetal kidney II"
/dev_stage="Fetus"
/note="Organ: Kidney; Vector: pBluescript KS-; Site_1:
XhoI; Site_2: EcoRI"
XhoI; 88 c 95 g 88 t 3 others
BASE COUNT 63 a 88 c 95 g
ORIGIN
Query Match 100.0%; Score 35; DB 32; Length 337;
Best Local Similarity 100.0%; Pred. NO. 1.1;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gactcgagtcgacatcgatttttttttttttttttt 35
|||||
Db 4 GACTCGAGTCGACATCGATCGATTTT TTTT TTTT 38

RESULT 2
AI295887/c 678 bp mRNA EST 01-DEC-1998
LOCUS LP09649.5prime LP Drosophila melanogaster larval-early pupal p0n2
DEFINITION Drosophila melanogaster cDNA clone LP09649 5prime, mRNA sequence.
ACCESSION AI295887
NID 93945294
VERSION AI295887.1 GI:3945294
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 111)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Feb 10, 1998 this sequence version replaced gi:2340789.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 678)
Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
Brokstein,P., Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:2044369.

Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 96 row: E column: 1
High quality sequence stop: 635.
Location/Qualifiers
1. .678
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="LP09649"
/p0n2"
/sex="male and female"
/dev_stage="larvae-pupae"
/lab_host="DH5-alpha"
/note="Organ: whole body; Vector: p0n2; Site_1: EcoRI;
Site_2: XhoI; Sized fractionated cDNAs were directly
ligated into p0n2. Plasmid cDNA library.
BASE COUNT 204 a 178 c 154 g 142 t
ORIGIN
Query Match 73.1%; Score 25.6; DB 44; Length 678;
Best Local Similarity 87.5%; Pred. NO. 2e+02;
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 tcgaatcgacatcgatttttttttttttttttttttt 35
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Db 621 TCCATTCGACCTCGAGTTT TTTT TTTT TTTT 590

RESULT 3
AI312326/c 111 bp mRNA EST 14-DEC-1998
LOCUS ta78e03.x2 NCI-CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050204 3',
DEFINITION mRNA sequence.
ACCESSION AI312326
NID 94017931
VERSION AI312326.1 GI:4017931
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 111)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Feb 10, 1998 this sequence version replaced gi:2340789.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

```


RESULT	8	EST	02-OCT-1996
C18175/c			
LOCUS			
DEFINITION			
	C18175	435 bp	EST
	C18175	Human placenta cDNA (TFujiwara)	Homo sapiens cDNA clone
	GEN-558E05	5' mRNA sequence.	

```

FEATURES                                Location/Qualifiers
1. .466
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/map="1q"
/clone="UI-R-Y0-acg-b-01-0-UI"
/clone_lib="UI-R-Y0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
note=vector: pMT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-Y0
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,
UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dt track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-Y0) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTs had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B

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www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 389      Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 273.
Location/Qualifiers
1..314
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:982855"
/clone_lib="NCI_CGAP_Pr12"
/sex="male"
/tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
/note="Vector: pAMP10; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
NIH."
BASE COUNT    97 a   52 c   65 g   100 t
ORIGIN

Query Match          70.3%; Score 24.6; DB 35; Length 314;
Best Local Similarity 87.1%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 cgatcgacatgcattttttttttttttttt 35
||||| ||||| ||||| ||||| ||||| |||||
Db 313 CGCGTCGACCTTCATTTTTTTT 283


RESULT 10
A1726205          466 bp      mRNA      EST      11-JUN-1999
BNLGH15252 Six-day Cotton fiber Gossypium hirsutum CDNA 5' similar
to (Y09741) beta-tubulin 1 [Hordeum vulgare], mRNA sequence.
A1726205
ACCESSION
NID 95045057
VERSION A1726205.1 GI:5045057
KEYWORDS
SOURCE
ORGANISM
Gossypium hirsutum
upland cotton.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE
AUTHORS Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
TITLE ESTs from developing cotton fiber
JOURNAL Unpublished (1999)
COMMENT On May 18, 1998 this sequence version replaced gi:3137811.

Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burr@bnlxi.bnl.gov
Seq primer: T3 Primer.
Location/Qualifiers
1..466
/organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="Immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/note="Vector: pBluescript II KS+"
BASE COUNT    133 a   118 c   71 g   144 t
ORIGIN

C18175
NID 91579777
VERSION C18175.1 GI:1579777
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 435)
AUTHORS Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
Shinomiyama,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
Makawa,H., Nakamura,I. and Takahashi,E.
TITLE Otsuka cDNA project
JOURNAL Unpublished (1996)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1392743.

Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
Location/Qualifiers
1..435
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GEN-558E05"
/clone_lib="Human placenta cDNA (TFujiwara)"
/tissue_type="Placenta"
BASE COUNT    131 a   88 c   111 g   105 t
ORIGIN

Query Match          70.9%; Score 24.8; DB 28; Length 435;
Best Local Similarity 92.9%; Pred. No. 3.8e+02;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 gtcgacatgatctttttttttttttttt 35
||||| ||||| ||||| ||||| ||||| |||||
Db 274 GTGCACCTCGACTTTTTTTTTTTTTTTT 247


RESULT 9
AA541358/c       314 bp      mRNA      EST      19-AUG-1997
ni77d04.s1 NCI_CGAP_Pr12 Homo sapiens CDNA clone IMAGE:982855, mRNA
sequence.
ACCESSION AA541358
NID 92287792
VERSION AA541358.1 GI:2287792
KEYWORDS
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 314)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1394510.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuaiqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIN at:
```

[illegible]

Contact: Robert Strausberg, Ph.D.
Tel (301) 496-1350
Email: Robert.Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.linl.gov/db/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone. Original clone citation: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index. This read has been verified (found to hit its original self in the correct orientation)

Seq primer: -40RP from Gibco
High quality sequence stop: 417.

[illegible]

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:783502"
/clone_lib="NCI_CGAP_Pr2"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"

```

/note="Vector: pAMP10; Site_1: NotI; Site_2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from
 5,000-10,000 microdissected preneoplastic cells
 histologically-determined to be prostatic intraepithelial
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was
 ligated to EcoRI adaptors; 5 cycles of PCR applied to the
 cDNA with an adaptor-specific primer, and the resulting
 PCR product subcloned into pAMP10 by the UDG-cloning
 method (Life Technologies). Average insert size is 600
 bp. NOTE: Not directionally cloned. This library was
 constructed by David Krizman."

129 a	131 c	93 g	164 t
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BASE COUNT

ORIGIN

Query Match	69.7%	Score 24.4;	DB 51;	Length 517;
Best Local Similarity	82.4%	Pred. No. 4.5e+02;		
Matches 28; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY 2 actcgagtcacatcgcgattttttttttttttttttt 35
 | | | | | | | | |
Db 14 ATTCCGGCGGCGTCGATTTTttttttttttttttttt 47

RESULT	15
LOCUS	AAl45612
DEFINITION	m07h10.r1 stragene mouse skin (#937313); Mus musculus cDNA clone IMAGE:506307 5' similar to gb:x12953 RAS-RELATED PROTEIN RAB-2 (HUMAN); , mRNA sequence.
ACCESSION	AAl45612
NID	g1715011
VERSION	AAl45612.1
KEYWORDS	EST
SOURCE	house mouse
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 570) Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lucy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lenncon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1292118.

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:371739
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 347.
Location/Qualifiers
1. .570
source
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone_lib="IMAGE:606307"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTT 3'."

BASE COUNT 143 a 115 c 157 g 155 t
ORIGIN

Query Match 69.1%; Score 24.2; DB 29; Length 570;
Best Local Similarity 89.7%; Pred. No. 4.9e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 agtcgacatcgatttttttttttttttttt 35
|| ||||| ||||| ||||| ||||| |||||
Db 314 AGTCGACATCGAGTTTTTTTTTTTTTT 342

Search completed: October 1, 1999, 15:03:44
Job time: 4388 sec